

FIGURE 1A

(Map of Human IL-17 Receptor Like cDNA and Amino Acid Sequence)

(SEQ ID NO: 18 and SEQ ID NO:19)

```
ATCATGATCCCTATGGCCTGGCAGTAGGAATCTCCTGGGCTGGCGGGAGTTTGACAGCT 60
61 GTGGGGGCCATGAAGCGGGCAGAAAGAGAGGTGGATGATGTCCGGGGACTGGCATGACC 120
    * S G Q K E R W M S G D W H D P -
121 CTGGGTCACAGCAGTGCTGCTTGCAATTGGACTCCATGGGGCTTTGTGTGGAAGAGCAA 180
    G S Q Q C C L H L D S M G L C V G R A N -
181 ATTGGCTTCACTCTGCATCATGTTCTCTTGTGTTTCCACAGGGAGTGGGGCCAGCCAGCA 240
    W L H S A S C S L V F P Q G V G P A S R -
240 GAAACAGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACTTGAATC 300
    N S G L Y N I T F K Y D N C T T Y L N P -
301 CAGTGGGAAGCATGTGATTGCTGACGCCCCAGAAATATCACCATCAGCCAGTATGCTTGCC 360
    V G K H V I A D A Q N I T I S Q Y A C H -
361 ATGACCAAGTGGCAGTCACCATTTCTTGTGTCGCCCGGGCCCTCGGCATCGAATTCCTGA 420
    D Q V A V T I L W S P G A L G I E F L K -
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Inventor: Shuqian Jing

Title: "IL-17 Receptor Like Molecules and Uses Thereof"

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Fig. 1B

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FIGURE 1B

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421 AAGGATTTCGGGTAATACTGGAGGAGCTGAAGTCGGAGGGAAGACAGTGCCAACTGA 480
    G F R V I L E E L K S E G R Q C Q Q L I -
481 TTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAATCTCAAC 540
    L K D P K Q L N S S F K R T G M E S Q P -
541 CTTTCCTGAATATGAAAATTGAAACGGATTATTTCGTAAAGGTTGTCCCTTTTCCTTCCA 600
    F L N M K F E T D Y F V K V P P S I -
601 TTAAACGAAAGCAATTACCACCCTTCTTCTTTAGAACCCGAGCCTGTGACCTGTGTGT 660
    K N E S N Y H P F F F R T R A C D L L L -
661 TACAGCCGGACAATCTAGCTTGTAACCCCTTCTGGAAGCCTCGGAACCTGAACATCAGCC 720
    Q P D N L A C K P F W K P R N L N I S Q -
721 AGCATGGCTCGGACATGCAGGTGTCCTTCGACCACGACCGCACAACTTCGGCTTCCGTT 780
    H G S D M Q V S F D H A P H N F G F R F -
781 TCTTCTATCTTCACTACAAGCTCAAGCACGAAGACCTTTCAAGCGAAAGACCTGTAAGC 840
    F Y L H Y K L K H E G P F K R K T C K Q -
841 AGGAGCAAACTACAGAGATGACCAGCTGCCTCCTTCAAAATGTTTCTCCAGGGATTATA 900
    E Q T T E M T S C L L Q N V S P G D Y I -
901 TAATTGAGCTGTGGATGACACTAACACAACAAGAAAGTGATGATTCCTTAAAGC 960
    I E L V D D T N T T R K V M H Y A L K P -
```

FIGURE 1C

3721 GGGGGGCTTGCACCCCTGCTGGAAGAAAGGTTTGTGTATATTTCTGATGCAAAATGTCA 3780  
3781 TACTCACTGCTCTGTAAAGGCAGCTGCGCAGCTTTTGGGAAAAGAACGTGCTCGTCTGTGT 3840  
3841 CTCTGGCATCAAGTTTCTTGCAGCTGCTCTGAGGGAGAGACAGTGAGCTGCAAGACTGCC 3900  
3901 TCCCCATAACAACAGGCAACTCAGAGAAGAGTCAATTTTATGTTGTTCCCTATGGAATCTGG 3960  
3961 AATGAGTGCAGAGCTCCTACCCACACATGACTGCCCCGCCCATTTTCATCCTTAGGCATTCTG 4020  
4021 TGAAGGAGATTGGTTAGTCCAAACTTGCTAACATACGAAAAATTCACATTGGAACATGATGA 4080  
4081 GAGATTTCCTTATTGAGGCCAAGAGATGTTTCCTGTCCAGAGGAACCATTAGGAGTCGCT 4140  
4141 TTTAGGGTATTCAGCTTTGTTTCATGAAATAAGGCATCTCTGAGAAAGTGGCCCCAGGGAG 4200  
4201 AGAATGGAGGACTGGGAGGAGAACGATTAACTGAGCTCCAAGGGTGTGTGGCAGAGAGC 4260  
4261 TTGCTATGTGAACCTCACTCCTTAAGAAAAATGGAAGAGAAAAAGAGAGTCTAGTTAAAAA 4320  
4321 ATCGGGATGTTTTAGTTTGGATTTAGGGTTTGTGATACTTATGTTGAAATACTAATGTTTC 4380  
4381 TGATCAATAAAATCAAACTCTTAATAATACCGAGTAATGAAACCATAGTGTGATTGCCTCA 4440  
4441 GAATAAATTGAGAAAGTCCAAAAAATAAAAAAAAAAAAAAAAAAAAAA 4483

FIGURE 2A

Overlap of IL-17 Human Receptor-Like (hIL-17RL) Polypeptide and Known

Human IL-17 Receptor Family Member

(SEQ ID NO: 20)

hIL-17RL	MMSGDWHDPGSQQCCLHLDMSGLCVGRANWLHSASCSLVFPQGVGPASRN	50
Human IL-17R	..MGAARSPPS...AVPGPLLGLLLLLGVLAPGGASLRLLDHRALVCSQ	45
hIL-17RL	SGLYNITFKYDNC..TTYLNPVGKHVIADAQNITISQYACHDQ.....VA	93
Human IL-17R	PGL.NCTVKNSTCLDDSWIHP.RNLTSSPKDLQIQLHFAHTQQGDLFPV	93
hIL-17RL	VTILWS.PGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKR	142
Human IL-17R	AHIEWTLQTDASILYLEGAELSVLQNTNERLCVR..FEFLSKLRHHRR	141
hIL-17RL	TGMESQPFLNMKFETDYFVKV..VPFPSIKNESNYHPFFRTRACDLLLQ	190
Human IL-17R	WRFTFSHFV.VDPDQYEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARM	190
hIL-17RL	PDNLACK...PFWKPR.....NL.NISQHGSDMQVSFDHA	221
Human IL-17R	KVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHM	240

FIGURE 2B

hIL-17RL	PHNFGFRFFYLHYKLKHEGPFKRKTKCKQEQTTEMTSCLLQNVSPGDYIIE	271
Human IL-17R	ENHSCFEHMH.HIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFSS	289
hIL-17RL	LVDDT...NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFT	318
Human IL-17R	CLNDCLRHSATVSCPEMPDTPPIPDYMPPLWVYWFITGISILLVGSVILL	339
hIL-17RL	VMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRP...KVFLCYSS	364
Human IL-17R	IVCMTWRLAGPGS...EKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSA	386
hIL-17RL	KDQGNHMNVVQCFAFLQDFCGCEVALDLWEDFSLCREGQREWV.IQK..	411
Human IL-17R	DHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQE	435
hIL-17RL	.IHESQFIIVVCSKGMK...YFVDKKNYKHKGGRSGKGELFLVAVSA	456
Human IL-17R	MVESNSKIIIVLCSRGTAKWQALLGRGAPVRLRCDHKGKPVGDLFTAAMNM	485
hIL-17RL	IAEKLRLQAKQSSSAALSKFIAVVF.DYSCGDPVPGILDSTKYRLMDNLP	505
Human IL-17R	ILPDFKR....PACFGTYVVCYFSEVSCDGDVPDLFGAAPRYPLMDRFE	530

FIGURE 2C

hIL-17RL	QLCSHLHSRDHGLQEPGQHTRQG..SRRNYFRSKGRSLYVAICNMHQFI	553
Human IL-17R	EV..YFRIQDLEMFPQGRMHRVGEISGDNYLRSPPGGRQLRAALDRFRDWQ	578
hIL-17RL	DEEPDWFEEKQFV...PFHPPPLR...YREPVLEKFDGLVNDVMCKPG	596
Human IL-17R	VRCPDWFECENLYSADDQDAPSLDEEVFEELLP.P.GTGIVKRAPLVRE.	626
hIL-17RL	PESDFCLKVEAAVLGATGPADSQHE.....SQHGG	626
Human IL-17R	PGSQACLAIDPLVGEEGGAATAKLEPHLQPRGQAPQPLHTLVLAEEGA	676
hIL-17RL	LDQDGEARPALDGSAAALQPLLHTVKA...GSPSDMPRDSGIYDSSVPSS	672
Human IL-17R	LVAAVEPGPLADGAAVRLALAGEGEACPLLGSPPG.AGRNSVLF...LPVD	722
hIL-17RL	ELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPALPSKLLSSGSCKA	722
Human IL-17R	PEDSPL..GSSTPMASPDLLPEDVR.....EHLEGLMLSLFEQSLSCQA	764
hIL-17RL	DLGC.RSYTDELHAVAPL*	740
Human IL-17R	QGGCSRPAVMVLTDPHTPYEEEEQRQSVQSDQGYISRSSPQPEGLTEEMEE	814

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Fig. 3A

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**FIGURE 3A**

**Map of Human IL-17 Receptor Like cDNA and Amino Acid Sequences**

(SEQ ID NO: 1 and SEQ ID NO: 2)

TGGCTGGGCG AGCGCACGGC C 21

ATG GCC CCG TGG CTG CAG CTC TGC TCC GTC TTC TTT ACG GTC AAC 66

Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn

1 5 10 15

GCC TGC CTC AAC GGC TCG CAG CTG GCT GTC GCC GCT GGC GGG TCC 111

Ala Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser

20 25 30

GGC CGC GCG TGG GGC GTC GAC ACC TGT GGC TGG AGG GGA GTG GGG 156

Gly Arg Ala Trp Gly Val Asp Thr Cys Gly Trp Arg Gly Val Gly

35 40 45

CCA GCC AGC AGA AAC AGT GGG CTG TAC AAC ATC ACC TTC AAA TAT 201

Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr

50 55 60

FIGURE 3B

GAC AAT TGT ACC ACC TAC TTG AAT CCA GTG GGG AAG CAT GTG ATT	246
Asp Asn Cys Thr Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile	75
	70
GCT GAC GCC CAG AAT ATC ACC ATC AGC CAG TAT GCT TGC CAT GAC	291
Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp	90
	85
CAA GTG GCA GTC ACC ATT CTT TGG TCC CCA GGG GCC CTC GGC ATC	336
Gln Val Ala Val Thr Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile	105
	100
GAA TTC CTG AAA GGA GGA TTT CGG GTA ATA CTG GAG GAG CTG AAG TCG	381
Glu Phe Leu Lys Lys Gly Phe Arg Val Ile Leu Glu Glu Lys Ser	120
	115
GAG GGA AGA CAG TGC CAA CAA CTG ATT CTA AAG GAT CCG AAG CAG	426
Glu Gly Arg Gln Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln	135
	130
-CTC AAC AGT AGC TTC AAA AGA ACT GGA ATG GAA TCT CAA CCT TTC	471
Leu Asn Ser Ser Phe Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe	150
	145
	140



FIGURE 3C

CTG	AAT	ATG	AAA	TTT	GAA	ACG	GAT	TAT	TTC	GTA	AAG	GTT	GTC	CCT	516
Leu	Asn	Met	Lys	Phe	Glu	Thr	Asp	Tyr	Phe	Val	Lys	Val	Val	Pro	165
				155					160						
TTT	CCT	TCC	ATT	AAA	AAC	GAA	AGC	AAT	TAC	CAC	CCT	TTC	TTC	TTT	561
Phe	Pro	Ser	Ile	Lys	Asn	Glu	Ser	Asn	Tyr	His	Pro	Phe	Phe	Phe	
				170					175					180	
AGA	ACC	CGA	GCC	TGT	GAC	CTG	TTG	TTA	CAG	CCG	GAC	AAT	CTA	GCT	606
Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Leu	Gln	Pro	Asp	Asn	Leu	Ala	
				185					190					195	
TGT	AAA	CCC	TTC	TGG	AAG	CCT	CGG	AAC	CTG	AAC	ATC	AGC	CAG	CAT	651
Cys	Lys	Pro	Phe	Trp	Lys	Pro	Arg	Asn	Leu	Asn	Ile	Ser	Gln	His	
				200					205					210	
GGC	TCG	GAC	ATG	CAG	GTG	TCC	TTC	GAC	CAC	GCA	CCG	CAC	AAC	TTC	696
Gly	Ser	Asp	Met	Gln	Val	Ser	Phe	Asp	His	Ala	Pro	His	Asn	Phe	
				215					220					225	
GGC	TTC	CGT	TTC	TTC	TAT	CTT	CAC	TAC	AAG	CTC	AAG	CAC	GAA	GGA	741
Gly	Phe	Arg	Phe	Phe	Tyr	Leu	His	Tyr	Lys	Leu	Lys	His	Glu	Gly	
				230					235					240	

## FIGURE 3D

CCT TTC AAG CGA AAG ACC TGT AAG CAG GAG CAA ACT ACA GAG ACG	786
Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Glu Thr	255
	245
ACC AGC TGC CTC CTT CAA AAT GTT TCT CCA GGG GAT TAT ATA ATT	831
Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile	270
	260
	265
GAG CTG GTG GAT GAC ACT AAC ACA ACA AGA AAA GTG ATG CAT TAT	876
Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr	285
	275
	280
GCC TTA AAG CCA GTG CAC TCC CCG TGG GCC GGG CCC ATC AGA GCC	921
Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala	300
	290
	295
ATG GCC ATC ACA GTG CCA CTG GTA GTC ATA TCG GCA TTC GCG ACG	966
Met Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr	315
	305
	310
ETC TTC ACT GTG ATG TGC CGC AAG AAG CAA CAA GAA AAT ATA TAT	1011
Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr	330
	320
	325

FIGURE 3E

TCA	CAT	TTA	GAT	GAA	GAG	AGC	TCT	GAG	TCT	TCC	ACA	TAC	ACT	GCA	1056
Ser	His	Leu	Asp	Glu	Glu	Ser	Ser	Glu	Ser	Ser	Thr	Tyr	Thr	Ala	
335										340					345
GCA	CTC	CCA	AGA	GAG	AGG	CTC	CGG	CCG	CGG	CCG	AAG	GTC	TTT	CTC	1101
Ala	Leu	Pro	Arg	Glu	Arg	Leu	Arg	Pro	Arg	Pro	Lys	Val	Phe	Leu	
				350					355					360	
TGC	TAT	TCC	AGT	AAA	GAT	GGC	CAG	AAT	CAC	ATG	AAT	GTC	GTC	CAG	1146
Cys	Tyr	Ser	Ser	Lys	Asp	Gly	Gln	Asn	His	Met	Asn	Val	Val	Gln	
				365					370					375	
TGT	TTC	GCC	TAC	TTC	CTC	CAG	GAC	TTC	TGT	GGC	TGT	GAG	GTG	GCT	1191
Cys	Phe	Ala	Tyr	Phe	Leu	Gln	Asp	Phe	Cys	Gly	Cys	Glu	Val	Ala	
				380					385					390	
CTG	GAC	CTG	TGG	GAA	GAC	TTC	AGC	CTC	TGT	AGA	GAA	GGG	CAG	AGA	1236
Leu	Asp	Leu	Trp	Glu	Asp	Phe	Ser	Leu	Cys	Arg	Glu	Gly	Gln	Arg	
				395					400					405	
GAA	TGG	GTC	ATC	CAG	AAG	ATC	CAC	GAG	TCC	CAG	TTC	ATC	ATT	GTG	1281
Glu	Trp	Val	Ile	Gln	Lys	Ile	His	Glu	Ser	Gln	Phe	Ile	Ile	Val	
				410					415					420	

FIGURE 3F

GTT TGT TCC AAA GGT ATG AAG TAC TTT GTG GAC AAG AAG AAC TAC	1326
Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn Tyr	435
	425
	430
AAA CAC AAA GGA GGT GGC CGA GGC TCG GGG AAA GGA GAG CTC TTC	1371
Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe	450
	440
	445
CTG GTG GCG GTG TCA GCC ATT GCC GAA AAG CTC CGC CAG GCC AAG	1416
Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys	465
	455
	460
CAG AGT TCG TCC GCG GCG CTC AGC AAG TTT ATC GCC GTC TAC TTT	1461
Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe	480
	470
	475
GAT TAT TCC TGC GAG GGA GAC GTC CCC GGT ATC CTA GAC CTG AGT	1506
Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser	495
	485
	490
ACC AAG TAC AGA CTC ATG GAC AAT CTT CCT CAG CTC TGT TCC CAC	1551
Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His	510
	500
	505

FIGURE 3G

CTG CAC TCC CGA GAC CAC GGC CTC CAG GAG CCG GGG CAG CAC ACG	1596
Leu His Ser Arg Asp 515	Thr 525
	520
CGA CAG GGC AGC AGA AGG AAC TAC TTC CGG AGC AAG TCA GGC CGG	1641
Arg Gln Gly Ser Arg Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg	540
	530
	535
TCC CTA TAC GTC GCC ATT TGC AAC ATG CAC CAG TTT ATT GAC GAG	1686
Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu	555
	545
	550
GAG CCC GAC TGG TTC GAA AAG CAG TTC GTT CCC TTC CAT CCT CCT	1731
Glu Pro Asp Trp Phe Glu Glu Lys Gln Phe Val Pro Phe His Pro Pro	570
	560
	565
CCA CTG CGC TAC CGG GAG CCA GTC TTC GAG AAA TTT GAT TCG GGC	1776
Pro Leu Arg Tyr Arg Glu Glu Pro Val Leu Glu Lys Phe Asp Ser Gly	585
	575
	580
TTG GTT TTA AAT GAT GTC ATG TGC AAA CCA GGC CCT GAG AGT GAC	1821
Leu Val Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp	600
	590
	595

[illegible]

FIGURE 3I

TCC CTG ACG GAG AGC GTG TCC TCC TCT TCA GGC CTG GGT GAG GAG	2136
Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu	705
695	700
GAA CCT CCT GCC CTT CCT TCC AAG CTC CTC TCT TCT GGG TCA TGC	2181
Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys	720
710	715
AAA GCA GAT CTT GGT TGC CGC AGC TAC ACT GAT GAA CTC CAC GCG	2226
Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala	735
725	730
GTC GCC CCT TTG TAA C AAAACGAAAG AGTCTAAGCA TTGCCACTTT	2272
Val Ala Pro Leu End	
740	
AGCTGCTGCC TCCCTCTGAT TCCCCAGCTC ATCTCCCTGG TTGCATGGCC	2322
CACCTGGAGC TGAGGTCTCA TACAAGGATA TTTGGAGTGA AATGCTGGCC	2372
AGTACTTGTT CTCCCTTGCC CCAACCCTTT ACCGGATATC TTGACAAACT	2422
CTCCAATTTT CTAAATGAT ATGGAGCTCT GAAAGGCATG TCCATAAGGT	2472

FIGURE 3J

CTGACAAACAG CTTGCCAAAT TTGGTTAGTC CTTGGATCAG AGCCTGTTGT	2522
GGGAGGTAGG GAGGAAATAT GTAAAGAAAA ACAGGAAGAT ACCTGCACTA	2572
ATCATTCAGA CTTCAATTGAG CTCTGCAAAC TTTGCCCTGTT TGCTATTGGC	2622
TACCTTGATT TGAAATGCTT TGTGAAAAA GGCACCTTTA ACATCATAGC	2672
CACAGAAATC AAGTGCCAGT CTATCTGGAA TCCATGTTGT ATTGCAGATA	2722
ATGTTCTCAT TTATTTTGA TGTAGAATT ACATTGCCAT GGGTGTTAAA	2772
TAAGCTTTGA GTCAAAAGTC AAGAAAGTGA CTGAATATAC AGTCACCTTT	2822
TATGAAATGA AAAAAAAAAA AAAAAAAAAA AAAAAAGGC GGCCGCTCTA	2872
GAGTATCCCT CGAGGGGCC AAGCTTACGC GTACCCAGCT TTCTTGTA	2922
AAGTGTCCC TATAGTGAGT CGTATTATA GCTAGGCACT GGCCGTCGTT	2972
- TTACAACGTC GTGACTGGGA AACTGCCTAG CTTGGGATCT TTGTGAAGGA	3022
ACCTTACTTC TGTCGTGTGA CATAATTGA CAAACTACCT ACAGAGATTT	3072
AAAGCTCTAA G	3083

The predicted signal peptide is under-lined.



FIGURE 4A

Overlap of IL-17 Human Receptor Like Polypeptide (huIL-17RL; SEQ ID NO:2)  
and Known Human IL-17 Receptor Member (SEQ ID NO: 3)

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1 .....MAPWLQLCSVFFTVNACLNQSLAVAAGSGRARGADTC 39 huIL-17RL
      | | | . | | | . | | | . | | |
1 MGAARSPPSAVPGPLGLLLGLVLA.PGGASRLRL...DHRAL...VC 43 human IL-17R

40 GWRGVGPASRNSGLYNITFKYDNCCTTYLNPVGKHVIADAQNITISQYACH 89 huIL-17RL
      | . : | | . . . : | . | : . . |
44 SQPGLNCTVKNSTCLDDSWIHPRNLTSPSPKDLQI...QLHFAHTQQGD 90 human IL-17R

90 DQVAVTILWS.PGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNS 138 huIL-17RL
      | | | . | : | | . . . : | | . . . |
91 FPVA.HIEWTLQTDASILYLEGAELSVLQLNTNERLCVR..FEFLSKLRH 137 human IL-17R

139 SFKRTGMESQPFLNMKFETDYFVKV..VPFPSIKNESNYHPFFFRTRACD 186 huIL-17RL
      : | | . . : : | | | . | : : | :
138 HRRRWRTFSHFV.VDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCE 186 human IL-17R

187 LLLQPDNLACK...PFWKPR.....NL.NISQHGSDMQVS 217 huIL-17RL
      | | | | |
187 HARMKVTTPCMSSGSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTS 236 human IL-17R
```

FIGURE 4B

218	FDHAPHNFGFRFFYLHYKLKHEGPFKRKTKQEQTTMTSCLLQNVS	PGD	267	huIL-17RL
237	FPHMNHSCFEHMH.HIPAPRPEEFHORSNVTTLRLNLKGCCRHQVQIQP		285	human IL-17R
268	YIIELVDDT...NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVIS	AFA	314	huIL-17RL
286	FFSSCLNDCLRHSATVSCPMPDTPPEIPDYMPLWVYWFITGISILL	VGS	335	human IL-17R
315	TLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRP...	KVFL	360	huIL-17RL
336	VILLIVCMTWRLAGPGS...EKYSDDTKYTDGLPAADLIPPPLKPRK	VWI	382	human IL-17R
361	CYSSKDGQNHMNVVQCFAFLQDFCGCEVALDLWEDFSLCREGQRE	WV.I	409	huIL-17RL
383	IYSA.DHPLYVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVM	TWVGR	431	human IL-17R
410	QK...IHESQFIIVVCSKGMK...YFVDKKNYKHKGGRSGKGEL	FLV	452	huIL-17RL
432	QKQEMVESNSKIIVLCSRGTAKWQALLRGAPVRLRCDHGKPVGD	LFTA	481	human IL-17R
453	AVSAIAEKLROAKQSSSAALSKFIAVYF.DYSCGDVPGILDSTKY	RMLM	501	huIL-17RL
482	AMNMILPDFKR...PACFGTYVVCYFSEVSCDGDVDPDLFGAAP	RYPLM	526	human IL-17R

FIGURE 4C

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502 DNLPLQLCSHLHSRDHGLQEPGQHTRQG..SRRNYFRSKGRSLYVAICNM 549 huIL-17RL
    | :. : . | : :||. | | | | | | | | | | :
527 DRFEFV..YFRIQDLEMFQPGRMHRVGELSGDNYLRSFGGRQLRAALDRF 574 human IL-17R

550 HQFIDEEDWFEKQFV....PFHPPPLR...YREPVLEKFDLSGLVLNDVM 592 huIL-17RL
    . ||||| : . . | | | : ||. | . : | :
575 RDWQVRCPDWFECENLYSADDQDAPSLDEEVFEEPLLPP.GTGIVKRAPL 623 human IL-17R

593 CKPGPESDFCLKVEAAVLGATGPADSQHE.....S 622 huIL-17RL
    : | | | | : : | | | | | . . |
624 VRE.PGSQACLAIDPLVGEEGA AVAKLEPHLQPRGQPAPQPLHTLVLA 672 human IL-17R

623 QHGGLDQDGEARPALDGSAAALQPLLHTVKA....GSPDMPRDSGIYDSS 668 huIL-17RL
    : | | | | | | | | | . | | | | | | : :
673 EEGALVAAVEPGPLADGAAVRLALAGEGEACPLLGSFG.AGRNSVLF... 718 human IL-17R

669 VPSSELSPLMEGLSTDQTETSSLTESVSSSSGLGEEPPALPSKLLSSG 718 huIL-17RL
    . | | | | | | | | | | | | : |
719 LPVDPEDSPL..GSSTPMASPDLLPEDVR.....EHLEGLMLSLFEQSL 760 human IL-17R

719 SCKADLGC.RSYTDELHAVA PL*..... 740 huIL-17RL
    ||. | | | |
761 SCQAQGCSRPAMVLTDPHTPYEEEEQRQSVQSDQGYISRSSQPPEGLTE 810 human IL-17R
  
```

Percent Similarity: 34.286    Percent Identity: 26.429